OIPE

RAW SEQUENCE LISTING   DATE: 09/29/2003
PATENT APPLICATION: **US/10/663,401**   TIME: 14:36:33

Input Set : **N:\Crf3\RULE60\10663401.raw.txt**   **ENTERED**
Output Set: **N:\CRF4\09292003\J663401.raw**

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 1 <110> APPLICANT: CHEN, Hong
 2 <120> TITLE OF INVENTION: HUMAN GLUCOSE-6-PHOSPHATASE MOLECULES AND USES THEREOF
 3 <130> FILE REFERENCE: 10147-33U1
 4 <140> CURRENT APPLICATION NUMBER: US/10/663,401
 5 <141> CURRENT FILING DATE: 2003-09-16
 7 <150> PRIOR APPLICATION NUMBER: US/09/874,132
 8 <151> PRIOR FILING DATE: 2001-06-04
 9 <150> PRIOR APPLICATION NUMBER: US 09/586,511
10 <151> PRIOR FILING DATE: 2000-06-02
11 <160> NUMBER OF SEQ ID NOS: 27
12 <170> SOFTWARE: PatentIn Ver. 2.1
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 1138
16 <212> TYPE: DNA
17 <213> ORGANISM: Homo sapiens
18 <400> SEQUENCE: 1
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20      tccttcacag gaatggagtg ctcataattc agcatttgca gaaggactac cgagcttact 120
21      acactttttct aaattttatg tccaatgttg gagaccccag gaatatcttt ttcatttatt 180
22      ttccactttg ttttcaattt aatcagacag ttggaaccaa gatgatatgg gtagcagtca 240
23      ttggggattg gttaaatctt atatttaaat ggatattatt tggtcatcga ccttactggt 300
24      gggtccaaga aactcagatt tacccaaatc actcaagtcc atgccttgaa cagttcccta 360
25      ctacatgtga aacaggtcca ggaagtccat ctggccatgc aatgggcgca tcctgtgtct 420
26      ggtatgtcat ggtaaccgct gccctgagcc acactgtctg tgggatggat aagttctcta 480
27      tcactctgca cagactgacc tggtcatttc tttggagtgt tttttggttg attcaaatca 540
28      gtgtctgcat ctccagagta ttcatagcaa cacattttcc tcatcaagtt attcttggag 600
29      taattggtgg catgctggtg gcagaggcct ttgaacacac tccaggcatc caaacggcca 660
30      gtctgggcac atacctgaag accaacctct ttctcttcct gtttgcagtt ggcttttacc 720
31      tgcttcttag ggtgctcaac attgacctgc tgtggtccgt gcccatagcc aaaaagtggt 780
32      gtgctaaccc cgactggatc cacattgaca ccacgccttt tgctggactc gtgagaaacc 840
33      ttggggtcct cttttggcttg ggctttgcaa tcaactcaga gatgttcctc ctgagctgcc 900
34      gagggggaaa taactacaca ctgagcttcc ggttgctctg tgccttgacc tcattgacaa 960
35      tactgcagct ctaccatttc ctccagatcc cgactcacga agagcattta ttttatgtgc 1020
36      tgtctttttg taaaagtgca tccattcccc taactgtggt tgctttcatt ccctactctg 1080
37      ttcatatgtt aatgaaacaa agcggaaaga agagtcagta gaaaaaaaa aaaaaaa   1138
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 1065
41 <212> TYPE: DNA
42 <213> ORGANISM: Homo sapiens
43 <400> SEQUENCE: 2
44      atggatttcc ttcacaggaa tggagtgctc ataattcagc atttgcagaa ggactaccga 60
45      gcttactaca cttttctaaa ttttatgtcc aatgttggag accccaggaa tatctttttc 120
46      atttattttc cactttgttt tcaatttaat cagacagttg gaaccaagat gatatgggta 180
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```
47      gcagtcattg gggattggtt aaatcttata tttaaatgga tattatttgg tcatcgacct 240
48      tactggtggg tccaagaaac tcagatttac ccaaatcact caagtccatg ccttgaacag 300
49      ttccctacta catgtgaaac aggtccagga agtccatctg gccatgcaat gggcgcatcc 360
50      tgtgtctggt atgtcatggt aaccgctgcc ctgagccaca ctgtctgtgg gatggataag 420
51      ttctctatca ctctgcacag actgacctgg tcatttcttt ggagtgtttt ttggttgatt 480
52      caaatcagtg tctgcatctc cagagtattc atagcaacac attttcctca tcaagttatt 540
53      cttggagtaa ttggtggcat gctggtggca gaggcctttg aacacactcc aggcatccaa 600
54      acggccagtc tgggcacata cctgaagacc aacctctttc tcttcctgtt tgcagttggc 660
55      ttttacctgc ttcttagggt gctcaacatt gacctgctgt ggtccgtgcc catagccaaa 720
56      aagtggtgtg ctaaccccga ctggatccac attgacacca cgccttttgc tggactcgtg 780
57      agaaaccttg gggtcctctt tggcttgggc tttgcaatca actcagagat gttcctcctg 840
58      agctgccgag ggggaaataa ctacacactg agcttccggt tgctctgtgc cttgacctca 900
59      ttgacaatac tgcagctcta ccatttcctc cagatcccga ctcacgaaga gcatttattt 960
60      tatgtgctgt cttttttgtaa aagtgcatcc attcccctaa ctgtggttgc tttcattccc 1020
61      tactctgttc atatgttaat gaaacaaagc ggaaagaaga gtcag 1065
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63 <210> SEQ ID NO: 3
64 <211> LENGTH: 355
65 <212> TYPE: PRT
66 <213> ORGANISM: Homo sapiens
67 <400> SEQUENCE: 3

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68      Met Asp Phe Leu His Arg Asn Gly Val Leu Ile Ile Gln His Leu Gln
69       1               5                  10                  15
70      Lys Asp Tyr Arg Ala Tyr Tyr Thr Phe Leu Asn Phe Met Ser Asn Val
71                  20                  25                  30
72      Gly Asp Pro Arg Asn Ile Phe Phe Ile Tyr Phe Pro Leu Cys Phe Gln
73                  35                  40                  45
74      Phe Asn Gln Thr Val Gly Thr Lys Met Ile Trp Val Ala Val Ile Gly
75          50                  55                  60
76      Asp Trp Leu Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg Pro
77       65                  70                  75                  80
78      Tyr Trp Trp Val Gln Glu Thr Gln Ile Tyr Pro Asn His Ser Ser Pro
79                  85                  90                  95
80      Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser Pro
81                  100                 105                 110
82      Ser Gly His Ala Met Gly Ala Ser Cys Val Trp Tyr Val Met Val Thr
83                  115                 120                 125
84      Ala Ala Leu Ser His Thr Val Cys Gly Met Asp Lys Phe Ser Ile Thr
85                  130                 135                 140
86      Leu His Arg Leu Thr Trp Ser Phe Leu Trp Ser Val Phe Trp Leu Ile
87      145                 150                 155                 160
88      Gln Ile Ser Val Cys Ile Ser Arg Val Phe Ile Ala Thr His Phe Pro
89                  165                 170                 175
90      His Gln Val Ile Leu Gly Val Ile Gly Gly Met Leu Val Ala Glu Ala
91                  180                 185                 190
92      Phe Glu His Thr Pro Gly Ile Gln Thr Ala Ser Leu Gly Thr Tyr Leu
93                  195                 200                 205
94      Lys Thr Asn Leu Phe Leu Phe Leu Phe Ala Val Gly Phe Tyr Leu Leu
95          210                 215                 220
96      Leu Arg Val Leu Asn Ile Asp Leu Leu Trp Ser Val Pro Ile Ala Lys
```

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Input Set : N:\Crf3\RULE60\10663401.raw.txt
Output Set: N:\CRF4\09292003\J663401.raw

```
97      225                     230                     235                     240
98          Lys Trp Cys Ala Asn Pro Asp Trp Ile His Ile Asp Thr Thr Pro Phe
99                      245                 250                     255
100         Ala Gly Leu Val Arg Asn Leu·Gly Val Leu Phe Gly Leu Gly Phe Ala
101                     260                     265                 270
102         Ile Asn Ser Glu Met Phe Leu Leu Ser Cys Arg Gly Gly Asn Asn Tyr
103                     275                 280                     285
104         Thr Leu Ser Phe Arg Leu Leu Cys Ala Leu Thr Ser Leu Thr Ile Leu
105                     290                 295                     300
106         Gln Leu Tyr His Phe Leu Gln Ile Pro Thr His Glu Glu His Leu Phe
107         305                     310                     315                 320
108         Tyr Val Leu Ser Phe Cys Lys Ser Ala Ser Ile Pro Leu Thr Val Val
109                         325                 330                     335
110         Ala Phe Ile Pro Tyr Ser Val His Met Leu Met Lys Gln Ser Gly Lys
111                     340                 345                     350
112         Lys Ser Gln
113                 355
115 <210> SEQ ID NO: 4
116 <211> LENGTH: 355
117 <212> TYPE: PRT
118 <213> ORGANISM: Mus musculus
119 <400> SEQUENCE: 4
120         Met Asp Phe Leu His Arg Ser Gly Val Leu Ile Ile His His Leu Gln
121             1               5                   10                      15
122         Glu Asp Tyr Arg Thr Tyr Tyr Gly Phe Leu Asn Phe Met Ser Asn Val
123                     20                  25                      30
124         Gly Asp Pro Arg Asn Ile Phe Ser Ile Tyr Phe Pro Leu Trp Phe Gln
125                     35                  40                      45
126         Leu Asn Gln Asn Val Gly Thr Lys Met Ile Trp Val Ala Val Ile Gly
127             50                  55                      60
128         Asp Trp Phe Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg Pro
129         65                  70                      75                      80
130         Tyr Trp Trp Ile Gln Glu Thr Glu Ile Tyr Pro Asn His Ser Ser Pro
131                         85                  90                      95
132         Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser Pro
133                     100                 105                     110
134         Ser Gly His Ala Met Gly Ser Ser Cys Val Trp Tyr Val Met Val Thr
135                     115                 120                     125
136         Ala Ala Leu Ser Tyr Thr Ile Ser Arg Met Glu Glu Ser Ser Val Thr
137             130                 135                     140
138         Leu His Arg Leu Thr Trp Ser Phe Leu Trp Ser Val Phe Trp Leu Ile
139         145                 150                     155                     160
140         Gln Ile Ser Val Cys Ile Ser Arg Val Phe Ile Ala Thr His Phe Pro
141                         165                 170                     175
142         His Gln Val Ile Leu Gly Val Ile Gly Gly Met Leu Val Ala Glu Ala
143                     180                 185                     190
144         Phe Glu His Thr Pro Gly Val His Met Ala Ser Leu Ser Val Tyr Leu
145             195                 200                     205
146         Lys Thr Asn Val Phe Leu Phe Leu Phe Ala Leu Gly Phe Tyr Leu Leu
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Input Set : **N:\Crf3\RULE60\10663401.raw.txt**
Output Set: **N:\CRF4\09292003\J663401.raw**

```
147            210              215              220
148      Leu Arg Leu Phe Gly Ile Asp Leu Leu Trp Ser Val Pro Ile Ala Lys
149      225              230              235              240
150      Lys Trp Cys Ala Asn Pro Asp Trp Ile His Ile Asp Ser Thr Pro Phe
151                  245              250              255
152      Ala Gly Leu Val Arg Asn Leu Gly Val Leu Phe Gly Leu Gly Phe Ala
153                  260              265              270
154      Ile Asn Ser Glu Met Phe Leu Arg Ser Cys Gln Gly Glu Asn Gly Thr
155                  275              280              285
156      Lys Pro Ser Phe Arg Leu Leu Cys Ala Leu Thr Ser Leu Thr Thr Met
157                  290              295              300
158      Gln Leu Tyr Arg Phe Ile Lys Ile Pro Thr His Ala Glu Pro Leu Phe
159      305              310              315              320
160      Tyr Leu Leu Ser Phe Cys Lys Ser Ala Ser Ile Pro Leu Met Val Val
161                  325              330              335
162      Ala Leu Ile Pro Tyr Cys Val His Met Leu Met Arg Pro Gly Asp Lys
163                  340              345              350
164      Lys Thr Lys
165                  355
167 <210> SEQ ID NO: 5
168 <211> LENGTH:
169 <212> TYPE:
170 <213> ORGANISM:
171 <400> SEQUENCE: 5
W--> 172      000
174 <210> SEQ ID NO: 6
175 <211> LENGTH:
176 <212> TYPE:
177 <213> ORGANISM:
178 <400> SEQUENCE: 6
W--> 179      000
181 <210> SEQ ID NO: 7
182 <211> LENGTH:
183 <212> TYPE:
184 <213> ORGANISM:
185 <400> SEQUENCE: 7
W--> 186      000
188 <210> SEQ ID NO: 8
189 <211> LENGTH:
190 <212> TYPE:
191 <213> ORGANISM:
192 <400> SEQUENCE: 8
W--> 193      000
195 <210> SEQ ID NO: 9
196 <211> LENGTH:
197 <212> TYPE:
198 <213> ORGANISM:
199 <400> SEQUENCE: 9
W--> 200      000
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Input Set : N:\Crf3\RULE60\10663401.raw.txt
Output Set: N:\CRF4\09292003\J663401.raw

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        202 <210> SEQ ID NO: 10
        203 <211> LENGTH:
        204 <212> TYPE:
        205 <213> ORGANISM:
        206 <400> SEQUENCE: 10
W--> 207         000
        209 <210> SEQ ID NO: 11
        210 <211> LENGTH:
        211 <212> TYPE:
        212 <213> ORGANISM:
        213 <400> SEQUENCE: 11
W--> 214         000
        216 <210> SEQ ID NO: 12
        217 <211> LENGTH:
        218 <212> TYPE:
        219 <213> ORGANISM:
        220 <400> SEQUENCE: 12
W--> 221         000
        223 <210> SEQ ID NO: 13
        224 <211> LENGTH:
        225 <212> TYPE:
        226 <213> ORGANISM:
        227 <400> SEQUENCE: 13
W--> 228         000
        230 <210> SEQ ID NO: 14
        231 <211> LENGTH:
        232 <212> TYPE:
        233 <213> ORGANISM:
        234 <400> SEQUENCE: 14
W--> 235         000
        237 <210> SEQ ID NO: 15
        238 <211> LENGTH:
        239 <212> TYPE:
        240 <213> ORGANISM:
        241 <400> SEQUENCE: 15
W--> 242         000
        244 <210> SEQ ID NO: 16
        245 <211> LENGTH:
        246 <212> TYPE:
        247 <213> ORGANISM:
        248 <400> SEQUENCE: 16
W--> 249         000
        251 <210> SEQ ID NO: 17
        252 <211> LENGTH:
        253 <212> TYPE:
        254 <213> ORGANISM:
        255 <400> SEQUENCE: 17
W--> 256         000
        258 <210> SEQ ID NO: 18
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/29/2003
PATENT APPLICATION: **US/10/663,401**   TIME: 14:36:34

Input Set : **N:\Crf3\RULE60\10663401.raw.txt**
Output Set: **N:\CRF4\09292003\J663401.raw**

<u>Invalid Line Length:</u>
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 2

VERIFICATION SUMMARY   DATE: 09/29/2003
PATENT APPLICATION: **US/10/663,401**   TIME: 14:36:34

Input Set : **N:\Crf3\RULE60\10663401.raw.txt**
Output Set: **N:\CRF4\09292003\J663401.raw**

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L:172 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5)  SEQUENCE:
L:179 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (6)  SEQUENCE:
L:186 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7)  SEQUENCE:
L:193 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8)  SEQUENCE:
L:200 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9)  SEQUENCE:
L:207 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:214 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (11) SEQUENCE:
L:221 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (12) SEQUENCE:
L:228 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:
L:235 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (14) SEQUENCE:
L:242 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:
L:249 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:
L:256 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:263 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
L:270 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:277 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:
L:284 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (21) SEQUENCE:
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